

LIST OF SEQUENCES

(1) GENERAL INFORMATION:

(i) APPLICANT

(A) NAME: A.D.B.E.A.

ASSOCIATION POUR LE DEVELOPPEMENT DE LA  
BIOTHERAPIE EXPERIMENTALE ET APPLIQUEE  
HOPITAL SAINT VINCENT DE PAUL

(B) STREET: 74-82 AVENUE DENFERT ROCHEREAU

(C) CITY: PARIS

(E) COUNTRY: FRANCE

(F) POST CODE: 75674

(ii) TITLE OF THE INVENTION: PROTEINS HAVING LECTINIC  
PROPERTIES AND THEIR BIOLOGICAL APPLICATIONS

(iii) NUMBER OF SEQUENCES: 6

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version  
#1.30 (EPO)

(2) INFORMATION FOR SEQ. ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1831 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

09077506-03098

(B) LOCATION: 62..1469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

GAATTCGGC GAGTGCGCGC TCCTCCTCGC CCGCCGCTAG GTCCATCCCG GCCCAGCCAC	60
C ATG TCC ATC CAC TTC AGC TCC CCG GTA TTC ACC TCG CGC TCA GCC	106
Met Ser Ile His Phe Ser Ser Pro Val Phe Thr Ser Arg Ser Ala	
1 5 10 15	
GCC TTC TCG GGC CGC GGC GCC CAG GTG CGC CTG AGC TCC GCT CGC CCC	154
Ala Phe Ser Gly Arg Gly Ala Gln Val Arg Leu Ser Ser Ala Arg Pro	
20 25 30	
GGC GGC CTT GGC AGC AGC AGC CTC TAC GGC CTC GGC GCC TCG CGG CCG	202
Gly Gly Leu Gly Ser Ser Ser Leu Tyr Gly Leu Gly Ala Ser Arg Pro	
35 40 45	
CGC GTG GCC GTG CGC TCT GCC TAT GGG GGC CCG GTG GGC GCC GGC ATC	250
Arg Val Ala Val Arg Ser Ala Tyr Gly Gly Pro Val Gly Ala Gly Ile	
50 55 60	
CGC GAG GTC ACC ATT AAC CAG AGC CTG CTG GCC CCG CTG CGG CTG GGC	298
Arg Glu Val Thr Ile Asn Gln Ser Leu Leu Ala Pro Leu Arg Leu Gly	
65 70 75	
GCC GAC CCC TTC TCC CAG CGG GTG CGC CAG GAG GAG AGC GAG CAG ATC	346
Ala Asp Pro Phe Ser Gln Arg Val Arg Gln Glu Glu Ser Glu Gln Ile	
80 85 90 95	
AAG ACC CTC AAC AAC AAG TTT GCC TCC TTC ATC GAC AAG GTG CGG TTT	394
Lys Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe	
100 105 110	
CTG GAG CAG CAG AAC AAG CTG CTG GAG ACC AAG TGG ACG CTG CTG CAG	442
Leu Glu Gln Gln Asn Lys Leu Leu Glu Thr Lys Trp Thr Leu Leu Gln	
115 120 125	
GAG CAG AAG TCG GCC AAG AGC AGC CGC CTC CCA GAC ATC TTT GAG GCC	490
Glu Gln Lys Ser Ala Lys Ser Ser Arg Leu Pro Asp Ile Phe Glu Ala	
130 135 140	
CAG ATT GCT GGC CTT CGG GGT CAG CTT GAG GCA ATG CAG GTG GAT GGG	538
Gln Ile Ala Gly Leu Arg Gly Gln Leu Glu Ala Met Gln Val Asp Gly	
145 150 155	
GGC CGC CTG GAG CAG GGG CTG CGG ACG ATG CAG GAT GTG GTG GAG GAC	586
Gly Arg Leu Glu Gln Gly Leu Arg Thr Met Gln Asp Val Val Glu Asp	
160 165 170 175	
TTC AAG AAT AAG TAC GAA GAT GAA ATT AAC CGC CGC ACA GGT GCT GAG	634
Phe Lys Asn Lys Tyr Glu Asp Glu Ile Asn Arg Arg Thr Ala Ala Glu	
180 185 190	
AAT GAG TTT GTG GTC CTG AAG AAG GAT GTG GAT GCT GCC TAC ATG AGC	682
Asn Glu Phe Val Val Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Ser	
195 200 205	

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AAG GTG GAG CTG GAG GCC AAG GTG GAT GCC CTG AAT GAT GAG ATC AAC	730
Lys Val Glu Leu Glu Ala Lys Val Asp Ala Leu Asn Asp Glu Ile Asn	
210 215 220	
TTC CTC AGG ACC CTC AAT GAG ACG GAG TTG ACA GAG CTT CAG TCC CAG	778
Phe Leu Arg Thr Leu Asn Glu Thr Glu Leu Thr Glu Leu Gln Ser Gln	
225 230 235	
ATC TCC GAC ACA TCT GTG GTG CTG TCC ATG GAC AAC AGT CGC TCC CTG	826
Ile Ser Asp Thr Ser Val Val Leu Ser Met Asp Asn Ser Arg Ser Leu	
240 245 250 255	
GAC CTG GAC GGC ATC ATC GCT GAG GTC AAG GCG CAG TAT GAG GAG ATG	874
Asp Leu Asp Gly Ile Ile Ala Glu Val Lys Ala Gln Tyr Glu Glu Met	
260 265 270	
GCC AAA TGC AGC CGG GCT GAG GCT GAA GCC TGG TAC CAG ACC AAG TTT	922
Ala Lys Cys Ser Arg Ala Glu Ala Glu Ala Trp Tyr Gln Thr Lys Phe	
275 280 285	
GAG ACC CTC CAG GCC CAG GCT GGG AAG CAT GGG GAC GAC CTC CGG AAT	970
Glu Thr Leu Gln Ala Gln Ala Gly Lys His Gly Asp Asp Leu Arg Asn	
290 295 300	
ACC CGG AAT GAG ATT TCA GAG ATG AAC CGG GCC ATC CAG AGG CTG CAG	1018
Thr Arg Asn Glu Ile Ser Glu Met Asn Arg Ala Ile Gln Arg Leu Gln	
305 310 315	
GCT GAG ATC GAC AAC ATC AAG AAC CAG CGT GCC AAG TTG GAG GCC GCC	1066
Ala Glu Ile Asp Asn Ile Lys Asn Gln Arg Ala Lys Leu Glu Ala Ala	
320 325 330 335	
ATT GCC GAG GCT GAG GAG CGT GGG GAG CTG GCG CTC AAG GAT GCT CGT	1114
Ile Ala Glu Ala Glu Glu Arg Gly Glu Leu Ala Leu Lys Asp Ala Arg	
340 345 350	
GCC AAG CAG GAG GAG CTT GAA GCC GCC CTG CAG CGG GCC AAG CAG GAT	1162
Ala Lys Gln Glu Glu Leu Glu Ala Ala Leu Gln Arg Ala Lys Gln Asp	
355 360 365	
ATG GCA CGG CAG CTG CGT GAG TAC CAG GAA CTC ATG AGC GTG AAG CTG	1210
Met Ala Arg Gln Leu Arg Glu Tyr Gln Glu Leu Met Ser Val Lys Leu	
370 375 380	
GCC CTG GAC ATC GAG ATC GCC ACC TAC CGC AAG CTG CTG GAG GGC GAG	1258
Ala Leu Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu	
385 390 395	
GAG AGC CGG TTG GCT GGA GAT GGA GTG GGA GCC GCC AAT ATC TCT GTG	1306
Glu Ser Arg Leu Ala Gly Asp Gly Val Gly Ala Ala Asn Ile Ser Val	
400 405 410 415	
ATG AAT TCC ACT GGT GGC AGC AGC AGT GGC GGT GGC ATT GGC CTG ACC	1354
Met Asn Ser Thr Gly Gly Ser Ser Ser Gly Gly Gly Ile Gly Leu Thr	
420 425 430	

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CTC GGG GGA ACC ATG GGC AGC AAT GCC CTG AGC TTC TCC AGC AGT GCG 1402  
 Leu Gly Gly Thr Met Gly Ser Asn Ala Leu Ser Phe Ser Ser Ser Ala  
                   435                  440                  445

GGT CCT GGG CTC CTG AAG GCT TAT TCC ATC CGG ACC GCA TCC GCC AGT 1450  
 Gly Pro Gly Leu Leu Lys Ala Tyr Ser Ile Arg Thr Ala Ser Ala Ser  
                   450                  455                  460

CGC AGG AGT ACC CGC GAC TGAGTCGC CTCCCACCAC TCCACTCCTC 1496  
 Arg Arg Ser Thr Arg Asp  
                   465

CAGCCACCAC CCACAATCAC AGCCATTGCC GAGGCTGAGG AGTGTGGGGA GCTGGCGCTC 1556

AAGGATGCTC GTGCCAAGCA GGAGGAGCTG GAAGCCGCCC TGCAGCGGGC CAAGCAGGAT 1616

ATGGCACGGC AGCTGCGTGA GTACCAGGAA CTCATGAGCG TGAAGCTGGC CCTGGACATC 1676

GAGATCGCCA CCTACCGCAA GCTGCTGGAG GCGGAGGAGA GCCGGTTGGC TGGAGATGGA 1736

GTGGGAGCCG TGAATATCTC TGTGATGAAT TCCACTGGTG GCAGTAGCAG TGGCGGTGGC 1796

ATTGGGCTAG CCCTCGGGGG AACCATGGGC AGCAA 1831

(3) INFORMATION FOR SEQ. ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

ATG TCC ATC CAC TTC AGC TCC CCG GTA TTC ACC TCG CCG TCA GCC GCC 48  
 Met Ser Ile His Phe Ser Ser Pro Val Phe Thr Ser Arg Ser Ala Ala  
   1                  5                  10                  15

TTC TCG GGC CGC GGC GCC CAG GTG CGC CTG AGC TCC GCT CGC CCC GGC 96  
 Phe Ser Gly Arg Gly Ala Gln Val Arg Leu Ser Ser Ala Arg Pro Gly  
                   20                  25                  30

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GGC CTT GGC AGC AGC AGC CTC TAC GGC CTC GGC GCC TCG CGG CCG CGC	144
Gly Leu Gly Ser Ser Ser Leu Tyr Gly Leu Gly Ala Ser Arg Pro Arg	
35 40 45	
GTG GCC GTG CGC TCT GCC TAT GGG GGC CCG GTG GGC GCC GGC ATC CGC	192
Val Ala Val Arg Ser Ala Tyr Gly Gly Pro Val Gly Ala Gly Ile Arg	
50 55 60	
GAG GTC ACC ATT AAC CAG AGC CTG CTG GCC CCG CTG CGG CTG GGC GCC	240
Glu Val Thr Ile Asn Gln Ser Leu Leu Ala Pro Leu Arg Leu Gly Ala	
65 70 75 80	
GAC CCC TTC TCC CAG CGG GTG CGC CAG GAG GAG AGC GAG CAG ATC AAG	288
Asp Pro Phe Ser Gln Arg Val Arg Gln Glu Glu Ser Glu Gln Ile Lys	
85 90 95	
ACC CTC AAC AAC AAG TTT GCC TCC TTC ATC GAC AAG GTG CGG TTT CTG	336
Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu	
100 105 110	
GAG CAG CAG AAC AAG CTG CTG GAG ACC AAG TGG ACG CTG CTG CAG GAG	384
Glu Gln Gln Asn Lys Leu Leu Glu Thr Lys Trp Thr Leu Leu Gln Glu	
115 120 125	
CAG AAG TCG GCC AAG AGC AGC	405
Gln Lys Ser Ala Lys Ser Ser	
130 135	

(4) INFORMATION FOR SEQ. ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

Met Ser Ile His Phe Ser Ser Pro Val Phe Thr Ser Arg Ser Ala Ala	
1 5 10 15	
Phe Ser Gly Arg Gly Ala Gln Val Arg Leu Ser Ser Ala Arg Pro Gly	
20 25 30	

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Gly Leu Gly Ser Ser Ser Leu Tyr Gly Leu Gly Ala Ser Arg Pro Arg  
35 40 45

Val Ala Val Arg Ser Ala Tyr Gly Gly Pro Val Gly Ala Gly Ile Arg  
50 55 60

Glu Val Thr Ile Asn Gln Ser Leu Leu Ala Pro Leu Arg Leu Gly Ala  
65 70 75 80

Asp Pro Phe Ser Gln Arg Val Arg Gln Glu Glu Ser Glu Gln Ile Lys  
85 90 95

Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu  
100 105 110

Glu Gln Gln Asn Lys Leu Leu Glu Thr Lys Trp Thr Leu Leu Gln Glu  
115 120 125

Gln Lys Ser Ala Lys Ser Ser Arg Leu Pro Asp Ile Phe Glu Ala Gln  
130 135 140

Ile Ala Gly Leu Arg Gly Gln Leu Glu Ala Met Gln Val Asp Gly Gly  
145 150 155 160

Arg Leu Glu Gln Gly Leu Arg Thr Met Gln Asp Val Val Glu Asp Phe  
165 170 175

Lys Asn Lys Tyr Glu Asp Glu Ile Asn Arg Arg Thr Ala Ala Glu Asn  
180 185 190

Glu Phe Val Val Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Ser Lys  
195 200 205

Val Glu Leu Glu Ala Lys Val Asp Ala Leu Asn Asp Glu Ile Asn Phe  
210 215 220

Leu Arg Thr Leu Asn Glu Thr Glu Leu Thr Glu Leu Gln Ser Gln Ile  
225 230 235 240

Ser Asp Thr Ser Val Val Leu Ser Met Asp Asn Ser Arg Ser Leu Asp  
245 250 255

Leu Asp Gly Ile Ile Ala Glu Val Lys Ala Gln Tyr Glu Glu Met Ala  
260 265 270

Lys Cys Ser Arg Ala Glu Ala Glu Ala Trp Tyr Gln Thr Lys Phe Glu  
275 280 285

Thr Leu Gln Ala Gln Ala Gly Lys His Gly Asp Asp Leu Arg Asn Thr  
290 295 300

Arg Asn Glu Ile Ser Glu Met Asn Arg Ala Ile Gln Arg Leu Gln Ala  
305 310 315 320

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Glu Ile Asp Asn Ile Lys Asn Gln Arg Ala Lys Leu Glu Ala Ala Ile  
325 330 335

Ala Glu Ala Glu Glu Arg Gly Glu Leu Ala Leu Lys Asp Ala Arg Ala  
340 345 350

Lys Gln Glu Glu Leu Glu Ala Ala Leu Gln Arg Ala Lys Gln Asp Met  
355 360 365

Ala Arg Gln Leu Arg Glu Tyr Gln Glu Leu Met Ser Val Lys Leu Ala  
370 375 380

Leu Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu  
385 390 395 400

Ser Arg Leu Ala Gly Asp Gly Val Gly Ala Ala Asn Ile Ser Val Met  
405 410 415

Asn Ser Thr Gly Gly Ser Ser Ser Gly Gly Gly Ile Gly Leu Thr Leu  
420 425 430

Gly Gly Thr Met Gly Ser Asn Ala Leu Ser Phe Ser Ser Ser Ala Gly  
435 440 445

Pro Gly Leu Leu Lys Ala Tyr Ser Ile Arg Thr Ala Ser Ala Ser Arg  
450 455 460

Arg Ser Thr Arg Asp  
465

(5) INFORMATION FOR SEQ. ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

Met Ser Ile His Phe Ser Ser Pro Val Phe Thr Ser Arg Ser Ala Ala  
1 5 10 15

Phe Ser Gly Arg Gly Ala Gln Val Arg Leu Ser Ser Ala Arg Pro Gly  
20 25 30

Gly Leu Gly Ser Ser Ser Leu Tyr Gly Leu Gly Ala Ser Arg Pro Arg  
35 40 45

Val Ala Val Arg Ser Ala Tyr Gly Gly Pro Val Gly Ala Gly Ile Arg  
50 55 60

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Glu Val Thr Ile Asn Gln Ser Leu Leu Ala Pro Leu Arg Leu Gly Ala  
65 70 75 80  
Asp Pro Phe Ser Gln Arg Val Arg Gln Glu Glu Ser Glu Gln Ile Lys  
85 90 95  
Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu  
100 105 110  
Glu Gln Gln Asn Lys Leu Leu Glu Thr Lys Trp Thr Leu Leu Gln Glu  
115 120 125  
Gln Lys Ser Ala Lys Ser Ser  
130 135

(6) INFORMATION FOR SEQ. ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

Gly Leu Gly Ala Ser Arg Pro Arg Val Ala Val Arg Ser Ala Tyr  
1 5 10 15

(7) INFORMATION FOR SEQ. ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Asp Pro Phe Ser Gln Arg Val Arg Gln Glu Glu Ser Glu Gln Ile  
1 5 10 15

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